

$$; \quad \text{SH}_2\text{QUINCH} \quad \text{CHA}$$

1


```

STREET: 505 Pendocast Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
Z115: 94064

COMPUTER READABLE FORM:
METHOD TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Part of the release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475, 228A
FILING DATE: 06-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,946
FILING DATE: 17-SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,784
FILING DATE: 23-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN 1994
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 44,444
REFERENCE/JURIS NUMBER: 4660-0175, 21/G19PD2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 424-0800
TELEFAX: (415) 424-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYDROLYTICAL: NO
ORIGINAL SOURCE:
INITIATION ISOLATE: Human B cell leukemia/lymphoma 2
INITIAL ISOLATE: (del-2) proto-oncogene

```

```

Query March 1.6% Score 21.4; DB 27 Length 50;
Post Local Similarity 67.4%; Pred No. 9, 3e+03;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
cy 87 ccccccccccgcggcgacgagcctttcttgcgcgcgcgcgcctcg 135
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 cccccccccgcggcgacgagccttcctccgccgcgcgcgcgcgcgcg 50

RESULT 9
US OH 482 080A 174
Sequence 174, Application US/OH48Z080A
Patent No. 6010849

GENERAL INFORMATION:
APPLICANT: EDWARDS, Cynthia A.
APPLICANT: CARROLL, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: FRY, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genolabs Technologies, Inc.
STREET: 505 Remondrot Drive
CITY: Redwood City
STATE: CA

```

COUNTRY: USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,080A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0940
 INFORMATION FOR SEQ ID NO: 374:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
 INDIVIDUAL ISOLATE: (bc1-2) proto-oncogene

```

Query Match      1.6% ; Score 23.4 ; DB 3 ; length 50;
Best Local Similarity   67.3% ; Pred. No. 9.3e+03;
Matches    33; Conservative    0; Mismatches    16; Indels    0; Gaps    0;

OY      87 cgcceccgagcccccgagcacccttcctcggcccccccgtccg 135
          ||||| | | | | | | | | | | | | | | | | | | | |
DB       2 CCGCCCTTCCTCAGCCGCGGCCCGCCCGCGGCACGTCCCGCGCGG 50

RESULT 10
PCR-US93-12388-374
Sequence 374, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Genclabs Technologies, Inc.,
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```


Genototo version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd

OM nucleotide nucleotide search, using SW model

Run on: September 26, 2002, 09:00:36 : Search time 1767.99 Seconds

(without alignments)
11420.565 Million Cp1 updates/sec

Little: US-10-006-430-3

Sequence: 1 cccatgctgctggaagagcgc.....tgcctaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NDC
Gapop 10.0 : Gapext 1.0

Search: 13746237 seqs, 6748477542 residues

al number of hits satisfying chosen parameters: 888b2

Minimum DB seq length: 16
Maximum DB seq length: 50

Post processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

EST:*

1: em_est_bar:*

2: em_est_hum:*

3: em_est_int:*

4: em_est_mus:*

5: em_est_ov:*

6: em_est_pl:*

7: em_est_ro:*

8: em_est_tc:*

9: qb_est1:*

10: qb_est2:*

11: qb_est3:*

12: qb_est4:*

13: em_gss_hum:*

14: em_gss_int:*

15: em_gss_mus:*

16: em_gss_pl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42.4	2.2	49	10	Bf034637	Bf034637 Bf034637
2	27.6	1.8	50	12	A2456166	A2456166 IM0258820
3	24.6	1.6	48	9	AL637106	AL637106 AL637106
4	24.4	1.6	50	12	A2787456	A2787456 2M0033006
5	24.2	1.6	46	12	A2777521	A2777521 2M0012801
6	24.2	1.6	49	12	T643012P	A1453367 T. brucei
7	24.2	1.6	42	12	T643A10P	A1458255 T. brucei
8	24	1.6	48	12	A2646447	A2646447 IM0512A06
9	24	1.6	48	12	A2650456	A2650456 IM0520609
10	24	1.6	48	12	A2860712	A2860712 2M0166P18
11	24	1.6	49	12	A2506149	A2506149 IM0347005
12	24	1.6	49	12	A2656875	A2656875 IM0532M11
13	24	1.6	49	12	A2764533	A2764533 IM0560017
14	24	1.6	49	12	A2773388	A2773388 IM0584E23
15	24	1.6	49	12	A2828100	A2828100 2M0092A12
16	24	1.6	49	12	T61680390	A1474148 T. brucei
17	24	1.6	50	9	A120437	A120437 mm47A11.T

C 18	24	1.6	50	10	B1491464	B1491464 d10410.0
C 19	24	1.6	50	12	A2358097	A2358097 IM0100N08
C 20	24	1.6	50	12	A2816605	A2816605 2M0085K24
C 21	24	1.6	50	12	A2861629	A2861629 2M0166A19
C 22	24	1.6	50	12	A2967786	A2967786 2M0238F20
C 23	23.8	1.6	44	12	A342202	A342202 IM0075G11
C 24	23.8	1.6	44	12	A486433	A486433 IM0148N20
C 25	23.8	1.6	46	12	A2981881	A2981881 2M0264P23
C 26	23.6	1.6	44	12	AW332205	AW332205 SE10 AGS
C 27	23.6	1.6	48	12	A2652813	A2652813 IM0528N08
C 28	23.4	1.6	49	12	A2335579	A2335579 IM0065A01
C 29	23.2	1.6	43	10	B1667675	B1667675 603291024
C 30	23	1.5	47	12	A2597378	A2597378 IM0417C24
C 31	23	1.5	47	12	A2769421	A2769421 IM0570001
C 32	23	1.5	47	12	A2851459	A2851459 2M0154P07
C 33	22.8	1.5	43	12	A2407933	A2407933 IM0176G23
C 34	22.8	1.5	43	12	A2666812	A2666812 IM0547012
C 35	22.8	1.5	50	9	A0104216	A0104216 A0104216
C 36	22.6	1.5	50	9	AA574989	AA574989 vm4440.1
C 37	22.6	1.5	49	12	A2826077	A2826077 2M013A07
C 38	22.6	1.5	45	12	A2331900	A2331900 IM0360A03
C 39	22.6	1.5	45	12	A2442112	A2442112 IM0244K08
C 40	22.6	1.5	45	12	A2473613	A2473613 IM0289003
C 41	22.6	1.5	45	12	A2822082	A2822082 2M0095P05
C 42	22.6	1.5	46	12	A2325773	A2325773 IM0048112
C 43	22.6	1.5	46	12	A2407590	A2407590 IM0178A16
C 44	22.6	1.5	45	12	A2510203	A2510203 IM0354K06
C 45	22.6	1.5	46	12	A2650069	A2650069 IM0520I05

ALIGNMENTS

RESULT 1
LOCUS Bf034637
DEFINITION Bf034637 NIH Mochii normalized Xenopus neurula library Xenopus
ACCESSION Bf034637
VERSION Bf034637.1 GI:17392178
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Parelchthoptera; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 49)
Kiteyama, A., Terasaka, C., Mochii, M., Ueno, N., Shin, J. I., and Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
CONTACT: Tadashi Shin-I
NATIONAL INSTITUTE OF GENETICS
1111 Yata, Mishima, Shizuoka 411-8540, Japan
TEL: 81-559-81-6856
FAX: 81-559-81-6855
EMAIL: tshin@genes.nig.ac.jp.
LOCATION/Qualifiers
1. 49
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="Xf034637"
/clone_11p="NIH Mochii normalized Xenopus neurula library"
/tissue="type="whole embryo"
/dev_stage="stage 15"
10 a 10 g 16 t 1 others

Query Match 2.28, Score 32.4, DB 10, Length 49;
Host local Similarity 83.78, Prod. No. 2.1e-05;

TITLE	
JOURNAL COMMENT	Islam,H., Lomatoiu,S., Mahmood,M., Meenah,B., Pedersen,T.E., Kelly,J.M., Kosem,M., Kosem,K., Stokes,R., Jinye,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2009) Contact: Robert H. Weiss University of Utah Genome Center University of Utah Rm. 408 Biomedical Polymers Research Bldg., 20 S. 2010 E., SLG, UT 64112 USA Tel.: 801-583 5609 Fax: 801 583 7177 Email: rdunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 Row:A Column: 09 Seq primer: CAGTACCAAAATCATTTCCTCC Class: plasmid ends High quality sequence stop: 50. Location/Qualifiers: 1..50 /oranism=Mus musculus" /strain=MusHL/6a7" /lab.Xref=Taxon:10090" /-clone=FLOCZM0034006" /-contig.lib=Mouse 10kb plasmid UDCCJM library" /sec=Male" /job.host=E. coli strain XL10-gold, T1-resistant, F"- /mutE-Vectror:PMD42nv; Purified genomic DNA from M. musculinus c57Bl/6J (male) was obtained from the Jackson Laboratory Mouse Resource (http://www.jax.org/resources/documents/dnaref/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector PBD42nv(1) a copy-number <1 PMD42 (q1432134/bp/A132072.1). The vector was ligated into the derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and put into the shovred, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10 gold (Stratagene) cells and selected for ampicillin resistance."
CDS DEFINITION	0 aa 49 c 0 g 1 t
DNA DATA	
Query Match	1.6% Score 24.4 DB 12;
First Local Similarity	68.0%; Pval. No. 3.4e+06;
Mismatches	44; Conservative 0; Matches 16; Indels 0; Gaps 0.
Gy	R1 GTGGCGGC GGCGGTGGTGTTCTGCGGCCGCCG 130
Bb	TTTTTTTTTTT TTITTTT TT TT TTTTTT
A	CCCCCCCCTCCCCCCCCCCCTGCTGCTCCCGCCGCCGCCG 50
RESULT	
ASSEMBLY	
FEATURES	
DEFINITION	AZT77521 46 bp DNA linear GSS 16-FEB 2000
ACCSSION	ZM0012B01F Mouse 10k plasmid MUSCIM Library Mus musculinus genomic
VERSION	AZT77521 clone IMAGEZM012B01.F, DNA sequence.
KYWDKWS	AZT77521.1 GI:12906208
SOURCE	GSS
ORGANISM	House mouse. Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euarchontomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
REFERENCE	

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Robert B. Weiss
 University of Utah
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dhamn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0012 row B column 01
 Seq primer: CATTTCATAACGACGCGGACAT
 Class: plasmid ends
 High quality sequence stop: 46.
FEATURES
 Location/Qualifiers
 1..46
 /organism="Mus musculus"
 /strain="C57Bl/6J"
 /db_xref="taxon:10090"
 /clone="U00C2M0012401"
 /clone-lib="Mouse 10kb plasmid U00C2M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F⁺
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57Bl/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnars/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and 14
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 5.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g114732114) (pA129072-1), a copy number
 inducible derivative of plasmid R1. The vector was linearized
 with adaptors complementary to the insert adaptors and
 pulled. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

REFERENCE

1 (bases 1 to 49)

Hall, N., Bowman, S., Leonard, N.J., Joseph, J., Alkin, R., Chellumbarthi, S., Ormond, D., Harris, R., El Sayed, N., Hou, L., McVittie, S., Kapur, M., and Barrett, J.B.C.

JOURNAL

Tryptosoma brucei genome sequencing project. Sanger Centre, The Wellcome Trust genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrett@sanger.ac.uk and nll@sanger.ac.uk

COMMENT

Constructed at the Institute for Genome Research (IGR).

Tryptosoma brucei (FRED92/4 viral 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v. 3 method used for the library construction is described in detail in Smith, R. and Venter, J.C. (Makin small) insert libraries for whole genome shotgun sequencing projects. In genome sequencing: A practical approach, eds. M. Vanthin and R. Barrett, Oxford University Press, 1999).

Email: nll@sanger.ac.uk Details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/Projects/Tbrucei/>

RESULTS

Query Match 1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

Matches 42 Conservative 0 Mismatches 167 Indels 0 Gaps 0

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

Matches 42 Conservative 0 Mismatches 167 Indels 0 Gaps 0

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

Matches 42 Conservative 0 Mismatches 167 Indels 0 Gaps 0

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

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0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

Matches 42 Conservative 0 Mismatches 167 Indels 0 Gaps 0

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0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

Matches 42 Conservative 0 Mismatches 167 Indels 0 Gaps 0

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

Best Local Similarity 66.74% Ident. No. 3.7e-06

FEATURES

Location/Qualifiers

1..42

/organism="Tryptosoma brucei"

/strain="FRED92/4"

SOURCE

/db_xref="Taxon:5691"

/clone="6410"

/sex="Male"

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49

BASE COUNT

0 4 40 0 0 4 4 others

ORIGIN

1.00 Score 24.27 DB 12 Length 49



GeneCode version 4.5
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nm nucleotide nucleotide search, using SW model

Run on: September 26, 2002, 09:30:46, Search time 2781.42 seconds

(without alignments)
11255.437 Million cell updates/sec

Title: US-10-006-430-3
Feature: 1496
Sequence: 1 cctatgagctgctggagaaagcgc.....tgcctaaagaaaaa 1496

Scoring table:

IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 617836

Minimum DB seq length: 16
Maximum DB seq length: 50

Post processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: GenBank
1: gb|faa:*
2: gb|bq:*
3: gb|ba:*
4: gb|bna:*
5: gb|bav:*
6: gb|fat:*
7: gb|phi:*
8: gb|phi:*
9: gb|phi:*
10: gb|phi:*
11: gb|phi:*
12: gb|phi:*
13: gb|phi:*
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39: gb|phi:*
40: gb|phi:*
41: gb|phi:*
42: gb|phi:*
43: gb|phi:*
44: gb|phi:*
45: gb|phi:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result Query
No. Score Match Length DB ID

Description

C	1	38	2.5	50	6	AX204288	AX204288 Sequence
C	2	27	1.8	41	6	AX004402	AX004402 Sequence
C	3	26	1.7	38	6	AX004400	AX004400 Sequence
C	4	24.4	1.6	50	6	AR032719	AR032719 Sequence
C	5	24.4	1.6	50	6	129459	129459 Sequence
C	6	24.4	1.6	50	6	191133	191133 Sequence
C	7	23.8	1.6	49	6	121777	121777 Sequence
C	8	23.4	1.6	50	6	AP043262	AP043262 Sequence
C	9	23.4	1.6	50	6	129502	129502 Sequence
C	10	23.4	1.6	50	6	191176	191176 Sequence
C	11	23	1.5	38	6	AX040139	AX040139 Sequence
C	12	22.8	1.5	49	6	AR162086	AR162086 Sequence
C	13	22.8	1.5	49	6	AR166611	AR166611 Sequence
C	14	22.8	1.5	50	9	HSILX1A4	HSILX1A4 Sequence
C	15	22.6	1.5	45	6	AX235169	AX235169 Sequence
C	16	22.4	1.5	49	6	AR032655	AR032655 Sequence
C	17	22.4	1.5	49	6	129395	129395 Sequence
C	18	22.4	1.5	49	6	191069	191069 Sequence
C	19	22.2	1.5	43	6	AP110219	AP110219 Sequence
C	20	22.2	1.5	43	6	AR169978	AR169978 Sequence
C	21	22.2	1.5	43	6	AR171787	AR171787 Sequence
C	22	22.2	1.5	43	6	AR068140	AR068140 Sequence
C	23	22.2	1.5	47	6	AR8774	AR8774 Sequence
C	24	22	1.5	43	6	AR162088	AR162088 Sequence
C	25	22	1.5	43	6	AR166613	AR166613 Sequence
C	26	22	1.5	50	6	AX199554	AX199554 Sequence
C	27	21.8	1.5	50	6	AR137495	AR137495 Sequence
C	28	21.4	1.4	47	6	AX068134	AX068134 Sequence
C	29	21.4	1.4	47	6	AX244094	AX244094 Sequence
C	30	21.2	1.4	31	6	AX244094	AX244094 Sequence
C	31	21.2	1.4	46	6	AR162087	AR162087 Sequence
C	32	21.2	1.4	46	6	AR166612	AR166612 Sequence
C	33	21	1.4	49	6	AR166612	AR166612 Sequence
C	34	21	1.4	50	6	AX165817	AX165817 Sequence
C	35	20.8	1.4	42	6	AX050342	AX050342 Sequence
C	36	20.8	1.4	42	6	AX317357	AX317357 Sequence
C	37	20.8	1.4	42	6	AX317358	AX317358 Sequence
C	38	20.6	1.4	35	6	135032	135032 Sequence
C	39	20.6	1.4	43	6	AR162088	AR162088 Sequence
C	40	20.6	1.4	43	6	AR166613	AR166613 Sequence
C	41	20.6	1.4	46	6	AR162087	AR162087 Sequence
C	42	20.6	1.4	46	6	AR166612	AR166612 Sequence
C	43	20.6	1.4	48	6	AR066468	AR066468 Sequence
C	44	20.6	1.4	49	6	AR162086	AR162086 Sequence
C	45	20.6	1.4	49	6	AR166611	AR166611 Sequence

ALIGNMENTS

RESULT 1
AX204288/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORIGINISM
human
Homo sapiens
Eukaryota; Metazoa; Chordata; Cephalata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
SHIMKETS, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0148245-A 394 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26"

Misc_Feature

